

IN THE CLAIMS

In accordance with the revised format for claim amendments, all claims are shown below. Please amend the claims as follows:

1. (Currently Amended) A composition comprising a substantially purified AviIII peptide, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme having at least 70% identity to SEQ ID NO. 3 and a carbohydrate binding domain (CBD) III, the catalytic domain GH74\_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (\*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AviIII\_Aace):

|            |   |
|------------|---|
| GH74_Ace   | ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPLLDWVG                  |
| AviIII_Aac | AASQAYTWKNNVTGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG                   |
|            | * : * . * * . * . * * * * . * * : * . * * * * * * ; : * * ; * * *             |
| GH74_Ace   | WNNWGNGVVSIAADPINTNKVWAAGVGMYTNSWDPNDGAILRSSDQGATWQITPLPFKLG                  |
| AviIII_Aac | NDTWHWDWGIDALATDPVTDTRVYAVGMYTNEWDPNVGSILRSTDQGDTWETKLPFKVG                   |
|            | : * * : ; : * : * : * : * : * . * * * * * * * * * : * * * : * * * * : *       |
| GH74_Ace   | GNMPGRGMGERLAVDPNNDNILYFGAPSGKGLWRSTDSGATWSQMTNFPDVGTYIANPTD                  |
| AviIII_Aac | GNMPGRGMGERLAVDPNKNISILYFGARSGHGLWKSTDYGATWSNVTSTWTGTYFQDSS                   |
|            | * * * * * * * * * : * . * * * * * * * * * : * . * . * * : * : * .             |
| GH74_Ace   | TTGYQSDIQGVVVVAFDKSSSLGQASKTIFVGVADPNNPVWSRDGGATWQAVPGAP-T                    |
| AviIII_Aac | T-T-YTSDPVGIAWVTFDSTSMSGGSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY                 |
|            | * * * * * : * . * * : * . * . * : * . * * * * * : * . * . * * : * . * *       |
| GH74_Ace   | GFIPHKGVFDPVNHLVYIATSNTPYDSSGDVWKFSVTSGTWRISPVPSSTDANDYF                      |
| AviIII_Aac | GFLPHKGVLSPEEKTLYISYANGAPYDGTNGTVHKYNITSGVWTDISP--TSLASTYY                    |
|            | * * : * * * * : * : * * : * : * . * * * * : * * : * * : * * * * * : * . * : * |
| GH74_Ace   | GYSGLTIDRQHPNTIMVATQISWWPTIIFRSTDGGATWTRIWDWTSTYPNRSLRYVLDIS                  |
| AviIII_Aac | GYGGLSDLQVPGTILMVAALNCWWPDELIFRSTDSGATWSPIWEWNGYPSINYYSYDIS                   |
|            | * * . * : * * . * : * * : * . * * * : * * * * . * * : * * . * * : * * * : * . |
| GH74_Ace   | AEPWLTFGVQPNPPVPSPKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTWDSGGQI                   |
| AviIII_Aac | NAPWIQDTTSTDQFP--VRVGWMVEALAIIDPFDSNHLYGTGLTVYGGHDLTNWDSKHNV                  |
|            | * * : * . . . : * : * * * * : * : * * * * : * : * : * * : * : * : * * : * :   |
| GH74_Ace   | HIAPMVGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTGV                   |
| AviIII_Aac | TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLDAAPNQAYHTPTYGTTNGI                  |
|            | : . . * : * * * * . * * : * * . * : * * : * * * * : * . : * : . * . . .       |
| GH74_Ace   | DYAELNPSIIVRAGSFDPSSQPNDRHVAFTDGGKNWFQGSEPGGVTTGGTVAASADGSR                   |
| AviIII_Aac | DYAGNPKPSNIVRSGASDDYP----TLALSSNFGSTWYADYAASTSTGTCAVALSADGDT                  |
|            | * * : * * * * : * . . . : * : * : * . . . * . * : * : * * * * .               |

|                        |  |
|------------------------|--|
| GH74_Ace<br>AviIII_Aac | FVWAPGDPGQPVVYAVGFGNSWAASQGVPANAQIRSDRVNPKTFYALSGNTFYRSTDGGV<br>VLLMSSTSGALVSKSQG---TLTAVSSLPSGAVIASDKSDNTVFYGGSAGAIYVSKNTAT<br>.: . . * * : * : : * . . * : * * : * . . * . * * : * . .           |
| GH74_Ace<br>AviIII_Aac | TFQPVAAGLPPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV<br>SFTKTVS-LGSSTTVNAIR-AHPSIAGDVASTDKGLWHSTDYGSTFTQIGSGVTAGWSF<br>: * . . * * : * . . * . . * * : * . . * * : * . . * : * . .        |
| GH74_Ace<br>AviIII_Aac | GFGKSAPGSSYPAVFVVGTTIGGVTGAYRSDDCGTTWVLINDDQHQYGN-WGQAITGDHAN<br>GFGKASSTGSYVVIYGFTTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVNGDLQT<br>*****: . . * . . : . * . . * . . ; * : * . . * . . * : * . . . . . |
| GH74_Ace<br>AviIII_Aac | LLRVYIGTNGRGIVYGDIGGAPSG<br>YGRVFRGHERPGHLLRQSQREPAG<br>***: * : * : : * ; * .   |

2. (Previously Amended) The composition of claim 1 wherein the AviIII peptide is further defined as comprising a linker and a signal sequence.
3. (Previously Cancelled)
4. (Previously Amended) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 80 to about 150 amino acids.
5. (Previously Amended) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 90 amino acids.
6. (Previously Amended) The composition of claim 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide sequence identical to SEQ ID NO: 3.
7. (Previously Amended) The composition of claim 1 wherein the carbohydrate binding domain (CBD) III is further defined as a polypeptide sequence of SEQ ID NO: 4.

8. (Previously Amended) The composition of claim 1 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.

9. (Currently Amended) The composition of claim 1 wherein said AviIII protein comprises sequences identical to the polypeptides of [-] SEQ ID NO: 3 and SEQ ID NO: 4.

10. (Currently Amended) The composition of claim 1, the catalytic domain GH74\_Ace including at least 90% sequence identity SEQ ID NO: 3.

11. (Previously Amended) The composition of claim 1 the catalytic domain GH74 including at least 80% sequence identity to SEQ ID NO: 3.

12. (Previously Amended) An isolated AviIII peptide having a polypeptide sequence of SEQ ID NO: 1.

13. (Previously Cancelled)

14. (Previously Amended) An industrial mixture suitable for degrading cellulose, such mixture comprising the AviIII polypeptide of claim 1.

15. (Original) The industrial mixture of claim 14 further defined as comprising a detergent.

28. (Previously Amended) An isolated polypeptide molecule comprising at least one polypeptide sequence selected from the group consisting of:

- a) a polypeptide sequence of SEQ ID NO: 3;
- b) a polypeptide sequence of SEQ ID NO: 4;
- c) a polypeptide sequence of SEQ ID NO: 5;

- d) a polypeptide sequence of SEQ ID NO: 1; and
- e) combinations thereof.

29. (Previously Cancelled)

30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

32. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.

33. (Previously Amended) The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemagglutinin, glutathione S-transferase, or OmpA signal sequence tag.

34. (Original) The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

35. (Original) The fusion protein of claim 34, wherein the agent is a leucine zipper.

36. (Original) A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 28 bound to cellulose.

43. (Original) A composition comprising the polypeptide molecule of claim 28 and a carrier.

44-46. (Previously Cancelled)